

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 02:14:44 ; Search time 36 seconds

(without alignments)
306.980 Million cell updates/sec

Title: US-09-308-829-2

Perfect score: 1232
Sequence: 1 MKKINIKIYFIITVLISF.....KDNRIIMKNFSDIYLEK 235

Scoring table: BIOSUM62

Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt.41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1182	95.9	235	1	SPEC_STPRY
2	394.5	32.0	234	1	SPEC_STPRY
3	219	17.8	258	1	ETXD_STAU
4	211	17.1	251	1	SPEA_STPRY
5	185.5	15.1	257	1	ETXE_STAU
6	183	14.9	266	1	ETCX_STAM
7	178.5	14.5	266	1	ETC2_STAU
8	177.5	14.4	257	1	ETXG_STAM
9	175	14.2	258	1	ETXG_STAM
10	171.5	13.9	266	1	ETXB_STAU
11	167.5	13.6	266	1	ETXB_STAU
12	142	11.5	236	1	SPEH_STPRY
13	96.5	7.8	910	1	NNOG_BUCAP
14	95	7.7	635	1	ETFL_YABAM
15	94	7.6	2077	1	TEGU_HSV6U
16	93.5	7.6	547	1	ZN81_HUMAN
17	93	7.5	541	1	FOH1_HAEIN
18	93	7.5	751	1	FOH1_PIG
19	91.5	7.4	430	1	YVCE_ECOLI
20	91	7.4	3343	1	YOG7_CAEEL
21	90.5	7.3	212	1	DSBA_BUCAI
22	90.5	7.3	948	1	RPOP_PODAN
23	90	7.3	715	1	UYRD_MYCPN
24	90	7.3	2077	1	TEGU_HSV6G
25	89	7.2	346	1	SYM_CHTUR
26	89	7.2	492	1	ATPB_PSTNU
27	89	7.2	569	1	CYSP_PLAFA
28	89	7.2	590	1	MP44_YUDY
29	89	7.2	670	1	PBP_STAU
30	87.5	7.1	831	1	RPOP_GEUSP
31	87.5	7.1	2869	1	RBP1_PLAYB
32	87	7.1	366	1	MURA_BUCAP
33	87	7.1	481	1	ATPB_MESVI

34	87	7.1	559	1	ENS2_YEAST
35	87	7.1	602	1	PEF2_LACIC
36	87	7.1	603	1	5NTD_HAEIN
37	86.5	7.0	432	1	Y221_METUA
38	86.5	7.0	463	1	SYC_MIGBR
39	86.5	7.0	1104	1	COLA_CLOPE
40	86	7.0	382	1	PORL_BUCAI
41	86	7.0	490	1	ATPB_CUSRE
42	86	7.0	492	1	ATPB_ANCLX
43	86	7.0	521	1	SYM_DREPA
44	86	7.0	524	1	Y395_MYCGE
45	86	7.0	792	1	Z328_HUMAN

ALIGNMENTS

RESULT 1	ID	SPEC_STPRY	STANDARD:	PRT:	235 AA.
AC	P13380:				
DT	01-JAN-1990 (Rel. 13, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	Exotoxin type C precursor (SPE C).				
GN	SPEC OR SPY0711.				
OS	Streptococcus pyogenes.				
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OX	Streptococcus.				
NCBI_TaxID=1314:					
RN	[1]				
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 28-52.				
RC	STRAIN-T18P / MGAS 1585.				
RX	MEDLINE=92363541; PubMed=1500157;				
RA	Kapur V., Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;				
RT	"Molecular population genetic evidence of horizontal spread of two				
RL	alleles of the pyrogenic exotoxin C gene (spec) among pathogenic				
RL	clones of Streptococcus pyogenes.";				
RL	Infect. Immun. 60:3513-3517(1992).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN-SF370 / ATCC 700294 / Serotype M1;				
RX	MEDLINE=21192684; PubMed=11296296;				
RA	Ferretti J.J., McShan W.M., Ajdic D.J., Savic G., Lyon K.,				
RA	Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,				
RA	Yuan Y., Jia H.G., Najaf F.Z., Ren Q., Zhu H., Song L., White J.,				
RT	"Complete genome sequence of an M1 strain of Streptococcus				
RT	pyogenes.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).				
RN	[4]				
RP	X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 30-235.				
RX	MEDLINE=97397352; PubMed=9253413;				
RA	Roussel A., Anderson B.F., Baker H.M., Fraser J.D., Baker E.N.;				
RT	"Crystal structure of the streptococcal superantigen SPE-C:				
RT	dimerization and zinc binding suggest a novel mode of interaction				
RT	with MHC class II molecules.";				
RL	Nat. Struct. Biol. 4:635-643(1997).				
CC	-I- SUBUNIT: Binds to major histocompatibility complex class II beta				
CC	chain.				
CC	-I- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE				
CC	THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET				
CC	FEVER. HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE				
CC	DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC				
CC	FEVER.				
CC	-I- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.				

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CC -! SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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CC -----
DR EMBL: M35514; AAA27017.1; ALT_SEQ.
DR EMBL: M97156; AAB59091.1; -.
DR EMBL: M97157; AAB59092.1; -.
DR EMBL: AE006523; AAK33664.1; -.
DR PIR: A30509; A30509.
DR PIR: A44799; A44799.
DR PDB: 1AN8; 29-APR-98.
DR PDB: 1KTK; 07-JUN-02.
DR InterPro: IPR006177; Bcstrl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF02876; Staph_stp_tox_C_1.
DR Pfam: PF01123; Staph_stp_toxin_1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Toxin; Signal; 3D-structure; Complete proteome.
FT CHAIN 1 28 235 EXOTOXIN TYPE C.
FT CONFLICT 53 53 N->D (IN REF. 1).
FT HELIX 33 44
FT STRAND 49 59
FT STRAND 63 67
FT STRAND 69 72
FT TURN 74 75
FT STRAND 77 81
FT HELIX 84 87
FT TURN 88 89
FT TURN 92 93
FT STRAND 95 100
FT TURN 108 109
FT STRAND 110 114
FT STRAND 117 119
FT STRAND 127 128
FT STRAND 131 135
FT TURN 136 137
FT STRAND 141 142
FT TURN 144 145
FT STRAND 148 149
FT STRAND 153 155
FT STRAND 156 171
FT HELIX 173 174
FT TURN 176 177
FT STRAND 182 189
FT TURN 190 191
FT STRAND 194 198
FT TURN 204 205
FT HELIX 208 212
FT STRAND 213 217
FT STRAND 220 222
FT HELIX 223 225
FT STRAND 226 235
SO SEQUENCE 235 AA; 27371 MM; 070534AAB952C1E0 CRC64;
Query Match 95.9%; Score 1182; DB 1; Length 235;
Best Local Similarity 97.0%; Pred. No. 7.5e-84;
Matches 228; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 1 MKKINIKIYVILITVILISTFTFYHOSDKKDINSVSDLLYATITIPYDKDORVNST 60
Db 1 MKKINIKIYVILITVILISTFTFYHOSDKKDINSVSDLLYATITIPYDKDORVNST 60

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QY 61 THTLNDIDQKYRGKDYIISSEMSYPASOKFRKRDHDVYGLPYILNSHGEYIGGTPA 120
Db 61 THTLNDIDQKYRGKDYIISSEMSYPASOKFRKRDHDVYGLPYILNSHGEYIGGTPA 120
QY 121 QNNKYNHKLGNLFTSGESQQLNNKILLEKDIYVFOEIDFKIRKYLMDNRYKYDATSPY 180
Db 121 QNNKYNHKLGNLFTSGESQQLNNKILLEKDIYVFOEIDFKIRKYLMDNRYKYDATSPY 180
QY 181 VSGRIEIGTKDGKHQDIDLFDSPNEGTSRSDIRAKKNDRIIMKNFSPHDYILEK 235
Db 181 VSGRIEIGTKDGKHQDIDLFDSPNEGTSRSDIRAKKNDRIIMKNFSPHDYILEK 235

RESULT 2
SPEC_STRPY STANDARD; PRT: 234 AA.
AC Q9XSC7;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Exotoxin type G precursor (SPE G).
GN SPEG OR SP10212.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-M1;
RA MEDLINE=99093428; PubMed=9874566;
RA Proft T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from
RL Streptococcus pyogenes.";
RN J Exp. Med. 189:89-102(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-SF370 / ATCC 700294 / Serotype M1;
RA MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -! SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain.
CC -! DISEASE: Mitogenic for human peripheral blood lymphocytes.
CC -! SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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CC -----
DR EMBL: AF124499; AAD30968.1; -.
DR EMBL: AE006489; AAK33303.1; -.
DR HSSP: P13380; 1AN8.
DR InterPro: IPR006177; Bcstrl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF02876; Staph_stp_tox_C_1.
DR Pfam: PF01123; Staph_stp_toxin_1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Toxin; Signal; Complete proteome.
FT SIGNAL 1 24 POTENTIAL.

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FO CHAIN      25       234          EXOTOXIN TYPE G.
FT SEQUENCE   234 AA; 27262 MW; 49525C49E4BA2052 CRC64;
Query Match           32.0%; Score 394.5; DB 1; Length 234;
Best Local Similarity 38.0%; Pred. No. 1,7e-23;
Matches 87; Conservative % 54; Mismatches 81; Indels 7; Gaps 5;

OY 12 IIVVILSTFFTY--HSDSKDLSNNKSDLLVATYTTPDPYKKCRNRFSTHTLINDTD 69
    :|::||::| |::| ::::|::| || |::| ::::|::|:
DB 5 ILTVILSCVFSGSLAYADENLKDKRSIRFAYNTPCDYEVETAFVTNSIHINTK 64
    :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 70 KYRGR-DVIYSSEMSYEASQKFRDDHDVDGFLYLINSHGXYIGGITPAON--NKVN 126
    :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 65 QKRBCCLLYDSIYSLGTDFQFIGDAVDVDFGLPYNSSPVDNIYGGIYKHSNQNK-S 123
    :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 127 HKLLGNLFISGESQQLNNKIILEKDIYTFQEIDFKIRKYLMDNYKYIADATSPVSGRIE 186
    :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 124 LQFGILINQDGKEITYLSEAVRIKKOFLOEPFKIRKFLMEKYNINYDESRYTSGSLF 183
    :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY 187 IGTWDGHEQIDLFDPSFNE-CTRSDIFRAKYDNKIIIMKNSSHDIYLE 234
    :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB 184 LATPKDSRHYEVDLFNKKDKLLSRDSFPKRYKDKNFNSEISHPDYLYK 232
    :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 3
ETXD_STAUB STANDARD: PRT; 258 AA.
AC P20723;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Enterotoxin type D precursor (SED).
GN ENTD.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
[1]
RP SEQUENCE FROM N.A., PubMed-89359112; PubMed-2549000;
RN MEDLINE-89359112; PubMed-2549000;
RA Bayles K.W., Iandolo J.J.;
RT "Genetic and molecular analyses of the gene encoding staphyloccocal enterotoxin D.";
RL J. Bacteriol. 171:4799-4806(1989).
[2]
RN SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RP STRAIN-ATCC 23235;
RC MEDLINE-97157473; PubMed-9003758;
RX Sundstroem M., Abrahamson L., Antonsson P., Mehlnade K., Mourad W.,
RA Dohlsten M.;
RT "The crystal structure of staphylococcal enterotoxin type D reveals Zn2+-mediated homodimerization.";
RL EMBO J. 15:6832-6840(1996).
CC -1 SUBUNIT: HOMODIMER: ZINC-DEPENDENT.
CC -1 SUBCELLULAR LOCATION: Secreted.
CC -1 DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC STAPHYLOCOCCAL TOXIN FAMILY.
CC -1 SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN FAMILY.
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CC -----
DR EMBL; M28521; AAB06195.1; -.
DR PIR; A33953; A33953.
DR HSSP; P13163; 1SXZ.
DR InterPro; IPR0006177; Betrl_tox.
DR InterPro; IPR0006123; Staph/Strep_toxin.
DR InterPro; IPR0006126; Staph/Strept_tox.

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DR InterPro:IPR006173; Staph_tox_OB.
DR Pfam: PF02876; Staph_Strp_tox_C: 1.
DR Pfam: PF01123; Staph_Strp_toxin: 1.
DR PRINTS: PR00279; BACTRLOTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1: 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2: 1.
DR Enterotoxin; Toxin; Signal; Superantigen; Zinc.
FT SIGNAL 1 25
FT CHAIN 26 258 ENTEROTOXIN TYPE D.
FT METAL 212 212 ZINC.
FT METAL 250 250 ZINC.
FT METAL 252 252 ZINC.
FT VARIANT 114 114 P->A (IN STRAIN AFCC 23235).
SQ SEQUENCE 258 AA; 29746 MW; 44706428D42597FD CRC64;

Query Match 17.8%; Score 219; DB 1; Length 258;
Best Local Similarity 26.3%; Pred. No. 5.3e-10;
Matches 75; Conservative 46; Mismatches 82; Indels 82; Gaps 12

QY 1 MKRNIKIVFIIIVILIS--TYTTTHOSDSKDD-----ISNVK----- 37
DB 1 MKKENIILALDFETSLVISPUNKANENIDSVKEELHKKSESLSTALNNMKHASYADNP 60
QY 38 -----SDLIYATIPR-VYDKCRVNEFSTHRLNIDTQYRGDYISSEM 82
DB 61 IIGENKSTGDOFLENTLLYKKFETDLINFDLLINFN----- 97
QY 83 SEYASQKFRKRDHVDVEGLFYILNSHNGEY-----IYGITPAQNNKYNH--KLGNLFI 135
DB 98 SKEMAQHFK-SKNVDYPIRISINCYSGEIDRTACTGYGVPHEBNKLEKKRKTITNIMI 156
QY 136 SGESQQLNNKKILLEKDIVTFQOEIDFKIRKYLMDNKKIYDATS---PYVSGRIEIGTKDG 192
DB 157 NGVQKEVSLDQVQDKKNVTQVQELDAQRRYRQLQDKLRYNDLTGKTIQPGKIEPDSIDG 216
QY 193 KHEIDIDFDSPNEGTRSDIPFK-----YQDNKILNNKNSHEDIYL 233
DB 217 SKVSYDLDFD-----VKGDPEPKOLRIYSDNKTLSTEHLL-HIDIYL 255

RESULT 4

SPEA_STRPY STANDARD: PRT: 251 AA.

AC P08095;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin) (SPE A).
GN SPEA OR SPYMA8_0393.
OS Streptococcus pyogenes, and
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
CX NCBI_TaxID=1314, 186103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86166804; PubMed=3514452;
RA Weeks C.R., Ferretti J.J.;
RT "Nucleotide sequence of the type A streptococcal exotoxin
RT (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
RT T12."
RL Infect. Immun. 52:144-150(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86284313; PubMed=3526093;
RA Johnson L.P., L'Italian J.J., Schlievert P.M.;
RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
RT related to Staphylococcus aureus enterotoxin B."
RL Mol. Gen. Genet. 203:354-356(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=MGAS8232 / Serotype M18;
OC

RX MEDLINE-21927593; PubMed-11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Yeasty L.G., Musser J.M.,
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
RX MEDLINE-99094887; PubMed-9878045;
RA Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,
RA O'Brien S.M., Trantler H.S., Acharya K.R.,
RT "Structural basis for the recognition of superantigen streptococcal
RT pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell
RT receptors";
RL EMBO J. 18:9-21(1999).
CC -1- SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain.
CC -1- DISEASE: THE STREPTOCOCCAL PYROGENIC TOXINS A, B, AND C ARE
CC THE CAUSATIVE AGENTS OF THE SYMPTOMS ASSOCIATED WITH SCARLET
CC FEVER, HAVE BEEN ASSOCIATED WITH STREPTOCOCCAL TOXIC SHOCK-LIKE
CC DISEASE AND MAY PLAY A ROLE IN THE EARLY EVENTS OF RHEUMATIC
CC FEVER.
CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
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CC -----
DR EMBL: U40453; AAC48668.1; -
DR EMBL: X03929; CA27568.1; -
DR EMBL: AE009982; AAL97141.1; -
DR PDB: 1B12; 24-NOV-99.
DR PDB: 1FNU; 17-NOV-00.
DR PDB: 1FNU; 17-NOV-00.
DR PDB: 1FNU; 17-NOV-00.
DR PDB: 1H45; 03-APR-02.
DR PDB: 1LOX; 03-APR-02.
DR InterPro: IPR006177; Bcrl1_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_08.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRLOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Toxin; Signal; 3D-structure; Complete proteome.
FT SIGNAL 1 30
FT CHAIN 31 251
FT DISULFID 117 128
FT FT
FT CONFLICT 6 6 K -> E (IN REF. 2).
FT CONFLICT 17 18 VT -> MK (IN REF. 2).
FT CONFLICT 25 35 SQEVAQDDP -> LFGGICSTRPK (IN REF. 2).
FT CONFLICT 40 40 H -> Q (IN REF. 2).
FT CONFLICT 43 43 S -> N (IN REF. 2).
FT CONFLICT 47 59 NLQNIYFLYEGDP -> TFKIYFFMRVTL (IN
FT REF. 2).
FT CONFLICT 129 129 I -> L (IN REF. 2).
FT CONFLICT 165 178 TNKKNVTHAQELDYK -> QINNGKCSRISTY (IN
FT REF. 2).
FT HELIX 36 38
FT HELIX 42 44
FT TURN 48 48
FT HELIX 49 56

FT STRAND 60 66
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 78
FT STRAND 82 82
FT TURN 83 84
FT STRAND 85 85
FT STRAND 87 91
FT HELIX 95 101
FT TURN 102 103
FT STRAND 105 110
FT STRAND 113 113
FT TURN 115 116
FT STRAND 126 130
FT STRAND 133 135
FT TURN 137 138
FT STRAND 140 153
FT TURN 154 155
FT STRAND 156 167
FT STRAND 169 171
FT HELIX 172 187
FT STRAND 199 205
FT STRAND 212 215
FT HELIX 224 227
FT TURN 228 231
FT TURN 232 233
FT STRAND 236 238
FT TURN 239 241
FT STRAND 243 249
SQ SEQUENCE 251 AA; 29246 MW; 54001FE4CCEBCC3 CRC64;

Query Match 17.1%; Score 211; DB 1; Length 251;
Best Local Similarity 27.8%; Pred. No. 2.1e-09;
Matches 72; Conservative 54; Mismatches 91; Indels 42; Gaps 14;

QY 2 KKNIIKIVFIIIVLISITFT-----YHSDSKKDISNKSDDLAVYITTP 48
DB 5 KKV-LKKNVFVFLVFLGLTISQEVFAQDDPDSQHLRSLVKNLONI-----YFLYEGDP 59
QY 49 YDXKDCR-VNFSTHTLNDIQKYGKDY-YISSFMSVSAQKFKRDHVDVFGI-FYIL 105
DB 60 VTHENVKSVDDLSHDLIYNVS--GPNYDKLTQLKQEMATLFRKDKNVYIGVEYHL 116
QY 106 ----NSHTGEIYIGITPAONNKVNH-----KLGNLFISGESQONLNKILIEKDIYV 155
DB 117 CYLCENARSAACIYGVV---NHGCHLEIKKIYVKKYSIDG--IQSLSPLEINKKAVT 171
QY 156 FOEIDFKIRKYLMDNKKIY-DATSPYVSGRIEIGTKDGKHQDILFDSNPGSTRSDIFAK 214
DB 172 AQELDYKVKRYLTDNKKQLYTNQPSKYETGYIKFIKKNKESFWDFEPPF-EFTQSKYIMI 230
QY 215 YKDNRIIMKNKFNSHDIYL 233
DB 231 YKDNETLD-SNISOIEVYL 248

RESULT 5
ENTRY STAAU STANDARD: PRT; 257 AA.
ID ENTRY STAAU STANDARD: PRT; 257 AA.
AC P12993;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Enterotoxin type E precursor (SEE).
GN ENTE.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_taxid=1280;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
RC STRAIN=MJ8265;
RX MEDLINE-88257005; PubMed-3384800;
RA Couch J.L., Solits M.T., Betley M.J.;

RT "Cloning and nucleotide sequence of the type E staphylococcal
RT enterotoxin gene.";
RL J. Bacteriol. 170:2954-2960(1988).
RN [2]
RP 3D-STRUCTURE MODELING:
RX MEDLINE=96022987; PubMed=7552730;
RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins.";
RL Nat. Struct. Biol. 2:680-686(1995).
CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M21319; AAA26617.1; -
CC PIR: A28179; A28179.
CC PDB: LSBE; 15-OCT-95.
DR InterPro: IPR006177; Bcrl1_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strept_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF02876; Staph_Strep_tox_C.1.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
KW 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 257
FT METAL 211 211 ENTEROTOXIN TYPE E.
FT METAL 249 249 ZINC (BY SIMILARITY).
FT METAL 251 251 ZINC (BY SIMILARITY).
FT METAL 251 251 ZINC (BY SIMILARITY).
FT HELIX 33 35
FT HELIX 39 41
FT STRAND 42 42
FT TURN 46 47
FT HELIX 48 51
FT HELIX 52 54
FT STRAND 59 64
FT TURN 66 67
FT STRAND 69 69
FT TURN 73 73
FT TURN 75 74
FT STRAND 77 79
FT TURN 83 84
FT STRAND 90 94
FT STRAND 98 104
FT HELIX 105 106
FT STRAND 109 113
FT STRAND 115 116
FT TURN 118 119
FT STRAND 128 132
FT STRAND 135 137
FT TURN 139 140
FT STRAND 142 142
FT STRAND 152 152
FT STRAND 154 155
FT TURN 156 157
FT STRAND 163 163
FT STRAND 171 171
FT STRAND 173 175

FT HELIX 176 190
FT TURN 191 191
FT STRAND 203 211
FT STRAND 219 221
FT STRAND 227 227
FT STRAND 234 239
FT HELIX 242 244
FT STRAND 245 247
FT TURN 249 257
SQ SEQUENCE 257 AA; 29358 MW; 27EDA94B97770CE3 CRC64;
Query Match 15.1%; Score 185.5; DB 1; Length 257;
Best Local Similarity 26.3%; Pred. No. 2e-07;
Matches 74; Conservative 45; Mismatches 87; Indels 75; Gaps 15;
QY 1 MKKINIKIVFITVLLISTFYTHOSDSKDIS-----NVSQSL-LIAY-- 44
DB 1 MKRTAFILLLFI-ALTLTSPLVNGSEKSEELNENDLRKSRLQNALSNLROIYYNE 58
QY 45 -TTPPYDKDCRY-----NESTTH-----TLNID-----TQYRGKDYISMSYE 85
DB 59 KATTEKESDDOPLNTLFLFKGFTGHFWYNDLVLDSKDATNKYKQ----- 107
QY 86 ASQKFKRDDHVDVFGLEFYILNSHTG-----EYIGGITPAONNNVNH--KLGMFLISGE 138
DB 108 -----KVDLYGAYYGQACGTPNKTACMYGCVTLHDNNRLTEKKVPIINLWIDCK 158
QY 139 SQONLNKKITLEDIYTFQEDIEFKIRKYLMDNKKIYDASPYVSGRIETG-----TKDK 193
DB 159 QTTVPIDKVKTSKREYVQELDQARHYLHGKFGLYNSDS--FGKRVQGLIVFHSSEGS 216
QY 194 HEQIDLFDSPNECTRSDFIAK-YKDNRIITNMKFSHFIDYL 233
DB 217 TVSYDLFDA--QGYPDTLIRIYRDKNTINSENL-HIDLYL 254
RESULT 6
ETC3_STAMM STANDARD; PRT; 266 AA.
ID ETC3_STAMM STANDARD; PRT; 266 AA.
AC P23313;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Enterotoxin type C-3 precursor (SEC3).
GN EMTC3 OR SAV2009 OR SA1817
OS Staphylococcus aureus (Strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (Strain N315), and
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; staphylococcus.
OX NCBI_TaxID=158878, 158879, 1280.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699, and N315;
RC MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuuchi J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=90220508; PubMed=2325627;
RA Hovde C.J., Hackelt S.P., Bohach G.A.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
RT sequence comparison of all three type C staphylococcal
RT enterotoxins.";
RL Mol. Gen. Genet. 220:329-333(1990).
RN [3]

[illegible]

DT	01-FEB-1994 (Rel. 28, Created)
DT	01-FEB-1994 (Rel. 28, Last sequence update)
DT	15-SEP-2003 (Rel. 42, Last annotation update)
DE	Enterotoxin type C-2 precursor (SEC2).
GN	ENTC2.
OS	Staphylococcus aureus.
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX	NCBI_TaxID=1280;
RN	[1]
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
RX	MEDLINE=89277549; Pubmed=2543637;
RA	Bohach G.A., Schlievert P.M.;
RT	"Conservation of the biologically active portions of staphylococcal enterotoxins C1 and C2."
RL	Infect. Immun. 57:2249-2252(1989).
RN	[2]
RP	X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX	MEDLINE=96027099; Pubmed=7582894.
RA	Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
RT	Brehm R.D., Tranter H.S.;
RL	"Crystal structure of the superantigen enterotoxin C2 from Staphylococcus aureus reveals a zinc-binding site."
RN	Structure 3:769-779(1995).
RN	[3]
RP	X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX	MEDLINE=96022987; Pubmed=7552730.
RA	Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
RT	"Residues defining V beta specificity in staphylococcal enterotoxins."
RL	Nat. Struct. Biol. 2:680-686(1995).
RN	[4]
RP	COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX	MEDLINE=97334373; Pubmed=9191070.
RA	Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT	"A structural and functional comparison of staphylococcal enterotoxins A and C2 reveals remarkable similarity and dissimilarity."
RL	J. Mol. Biol. 269:270-280(1997).
CC	-1- COPACATOR: Binds 1 zinc ion per subunit. The zinc ion is necessary for the toxin interaction with MHC class II.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION SYMPTHOMOCOCAL FOOD POISONING SYNDROME.
CC	-1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN FAMILY.
CC	PDB: A60114; A60114.
DR	PDB: 1STE; 23-DEC-96.
DR	PDB: 1SE2; 08-MAR-96.
DR	PDB: 1COV; 19-SEP-01.
DR	PDB: 1I4P; 19-SEP-01.
DR	PDB: 1I4Q; 19-SEP-01.
DR	PDB: 1I4R; 19-SEP-01.
DR	PDB: 1I4X; 19-SEP-01.
DR	InterPro: IPR006177; Bctrl_tox.
DR	InterPro: IPR006123; Staph/Strep_toxin.
DR	InterPro: IPR006126; Staph/Strep_tox.
DR	InterPro: IPR006173; Staph_tox_OB.
DR	Pfam: PF02876; Staph_Strep_tox_C; 1.
DR	Pfam: PF01123; Staph_Strep_toxin; 1.
DR	PRINTS: PR00279; BACTRLTOXIN.
DR	PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR	PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW	Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc; 3D-structure.
FT	SIGNAL
FT	CHAIN
FT	DISULFID
FT	METAL
FT	METAL
FT	METAL
FT	HELIX
FT	HELIX

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FT STRAND 44 44
FT TURN 48 48
FT HELIX 49 55
FT STRAND 60 65
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 79
FT TURN 83 86
FT STRAND 90 94
FT HELIX 98 104
FT TURN 105 106
FT STRAND 109 113
FT STRAND 116 116
FT TURN 118 119
FT TURN 128 129
FT STRAND 136 139
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FT STRAND 180 182
FT HELIX 183 198
FT STRAND 208 216
FT TURN 218 219
FT STRAND 222 226
FT STRAND 232 232
FT HELIX 237 241
FT HELIX 242 246
FT STRAND 249 251
FT TURN 252 254
FT STRAND 256 263
SQ SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;

Query Match 14.5%; Score 178.5; DB 1; Length 266;
Best Local Similarity 26.2%; Pred No. 7e-07;
Matches 65; Conservative 44; Mismatches 108; Indels 31; Gaps 9;

OY 6 IIRIVITVILISTYFYVHOSKSKRDISNVKSDLLVATTPYDKCRVMS----- 59
DB 10 VILIFALLIVLFTPNVLAESQDPDPDELHKSEFTGMKNKYLVDHYVATKMSVD 69
OY 60 --THTFL--NDTPQYRKQDYIISSEMSYASQKRRKRDHYVFGFLYLNH----- 108
DB 70 KFLADLILYNSDKRLKNYKTELNLMDLAKKTK-DEVVDVGSNYVNCYFSSKDNV 128
OY 109 --TG--EYIYGITPAQNNKVNHLGLNLFISGESQONLNKILF-----KDIYTFQEI 159
DB 129 GKVTOGKTCMVGITKIRHEGHNHFDNGNLQNLVLI--RYEKKRKTISFEVOTDKKSYTAQEL 186
OY 160 DKIRKYLMDNYKIVD-ATSPVSGRIETGDKGHEQIDLPDPSNEG--TRSDIFAKYKD 217
DB 187 DIKARNFLINKNLEYFNSSPYETGYIKFIENNGMTFWMDMAPAGDKFDQSKYLMKMYND 246
OY 218 NRILMKN 225
DB 247 NKTVDKS 254

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OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID-196620, 1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Nami T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RT Lancet 359:1819-1827(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FR137;
RX MEDLINE=88086892; PubMed=3335483;
RA Betley M.J., Mekalanos J.J.;
RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene."
RL J. Bacteriol. 170:34-41(1988).
RN [3]
RP SEQUENCE OF 25-257.
RX MEDLINE=8722293; PubMed=3584106;
RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
RT "Complete amino acid sequence of staphylococcal enterotoxin A."
RL J. Biol. Chem. 262:7006-7013(1987).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95354648; PubMed=7628431;
RA Schad E.M., Zaitseva I., Zaitsev V.N., Dohlstien M., Kalland T.,
RA Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
RT "Crystal structure of the superantigen staphylococcal enterotoxin
RT type A."
RL EMBO J. 14:3292-3301(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=97113025; PubMed=8943278;
RA Sundstroem M., Hallen D., Svensson A., Schad E., Dohlstien M.,
RA Abrahamson L.;
RT "The Co-crystal structure of staphylococcal enterotoxin type A with
RT Zn2+ at 2.7-A resolution. Implications for major histocompatibility
RT complex class II binding."
RL J. Biol. Chem. 271:32212-32216(1996).
RN [6]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96022987; PubMed=7552730;
RA Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
RT enterotoxins."
RL Nat. Struct. Biol. 2:680-686(1995).
RN [7]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE=97334373; PubMed=9191070;
RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT "A structural and functional comparison of staphylococcal
RT enterotoxins A and C2 reveals remarkable similarity and
RT dissimilarity."
RL J. Mol. Biol. 269:270-280(1997).
RN [8]
RP COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
RP for the toxin interaction with MHC class II.
RN [9]
RP SUBUNIT: Monomer.
RN [10]
RP SUBCELLULAR LOCATION: Secreted.
RN [11]
RP DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
RN STAPHYLOCOCCAL FOOD POISONING SYNDROME.
RN [12]
RP MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
RN [13]
RP SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
RN FAMILY.
RN [14]
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DR EMBL: AP004828; BAB95754.1; -

DR EMBL: M18970; AAA26681.1; -

DR PIR: A28664; A28664.

DR PDB: 1SEF; 11-JUL-96.

DR PDB: 1SXT; 19-NOV-97.

DR PDB: 1DYO; 21-FEB-02.

DR PDB: 1I4G; 21-MAR-01.

DR PDB: 1I4H; 21-MAR-01.

DR PDB: 1I0S; 18-DEC-02.

DR PDB: 1SEA; 15-OCT-95.

DR InterPro: IPR006177; Bcrl_tox.

DR InterPro: IPR006123; Staph/Strep_toxin.

DR InterPro: IPR006126; Staph/Strep_tox.

DR InterPro: IPR006173; Staph_tox_OB.

DR Pfam: PF02876; Staph_strep_tox_C; 1.

DR Pfam: PF01123; Staph_strep_toxin; 1.

DR PRINTS: PR00279; BACTRLTOXIN.

DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.

DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.

KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc; 3D-structure; Complete proteome.

FT STGNL 1 24

FT CHAIN 25 257 ENTEROTOXIN TYPE A.

FT DISULFID 120 130

FT METAL 211 211 ZINC.

FT METAL 249 249 ZINC.

FT METAL 251 251 ZINC.

FT CONFLICT 242 242 T -> S (IN REF. 3).

FT HELIX 28 31

FT TURN 32 33

FT HELIX 39 41

FT TURN 44 45

FT HELIX 46 55

FT TURN 56 56

FT STRAND 59 65

FT STRAND 69 69

FT TURN 73 74

FT STRAND 75 78

FT TURN 79 80

FT STRAND 90 94

FT HELIX 98 104

FT TURN 105 106

FT STRAND 108 116

FT TURN 118 119

FT TURN 125 126

FT STRAND 132 132

FT STRAND 135 137

FT TURN 139 140

FT STRAND 142 149

FT STRAND 151 155

FT TURN 156 157

FT STRAND 158 160

FT HELIX 164 166

FT STRAND 167 171

FT STRAND 173 175

FT HELIX 176 191

FT TURN 193 194

FT HELIX 197 199

FT TURN 200 200

FT STRAND 205 212

FT STRAND 221 221

FT TURN 222 223

FT HELIX 230 233

FT TURN 234 237

FT STRAND 238 239

FT STRAND 242 244

FT STRAND 248 255

SO SEQUENCE 257 AA; 29669 MW; ADBBFSBCALF14677 CRC64;

Query Match 14.4%; Score 177.5; DB 1; Length 257;

Best Local Similarity 26.8%; Pred. No. 8e-07;

Matches 63; Conservative 39; Mismatches 74; Indels 59; Gaps 13;

QY 24 YHSDSKKDISNVKSDLLVAVTI-----TPYD-YKCRNPFSTHTLNDTPKRYGKDY 76

Dd 54 YYNEKAKTENKESHQDFLOHTLFLFKGFTHDSNYNDLVDVFSKDIWD---KYRGK-- 107

QY 77 YISSEMSYEASQKFRDHDVDFGLFYILNSHTG-----EYIGGITPAQNNKVNH--KL 129

Dd 108 -----KVDLYGAYGYGACAGTTPKTCAGYGGVTLHDNNRLTEEKY 149

QY 130 LGNLFISGESQQLNKKIILE-----KDIYFPEIDFKIRKYIMDKYIDATSPYVSGR 184

Dd 150 PIVMLMDGK-----QNTVPLETVKTKNKNTVQVLDLQARKYLOEKYKYNYN--SDVFDGK 202

QY 185 IEIG-----TKDKHEDIDFDSNFGTREDIPAK-YKDRITMKNFHSFDIYL 233

Dd 203 VQGLIVFHTSTEPSVNYDLFGA--QGQYSNTILRLIRYRDKTKTINSENM-HIDITL 254

RESULT 9

ETXG_STAM STANDARD; PRT; 258 AA.

ID ETXG_STAM

AC 085382;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DE Enterotoxin type G precursor (SEG).

GN ENTG OR SEG OR SAV1824 OR SA1642.

OS Staphylococcus aureus (strain Mu50 / ATCC 700699),

OS Staphylococcus aureus (strain N315), and

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=158878, 158879, 1280;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN-FR1572.

RX MEDLINE=98298056; PubMed=9632603;

RA Munson S.H., Tremaine M.T., Beclay M.J., Welch R.A.;

RT Identification and characterization of staphylococcal enterotoxin

RT types G and I from Staphylococcus aureus.;

RL Infect. Immun. 66:3337-3348(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-Mu50 / ATCC 700699, and N315;

RX MEDLINE=21311952; PubMed=11418146;

RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

RA "Whole genome sequencing of methicillin-resistant Staphylococcus

RA aureus.;"

RL Lancet 357:1225-1240(2001).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION

CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.

CC -!- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN

CC FAMILY.

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CC or send an email to license@lsb-sib.ch).

CC EMBL: AF064773; AAC26660.1; -

DR EMBL: AP003363; BAB57986.1; -

DR EMBL: AP003135; BABA2910.1; -

DR PIR: G89968; G89968.


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DR HSSP: P01552; 1SB2.
DR InterPro: IPR006177; Bcrl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_08.
DR Pfam: PF02876; Staph_strep_tox_C; 1.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Enterotoxin; Toxin; Signal; Superantigen; Complete proteome.
FT SIGNAL 1 25
FT CHAIN 26 258 ENTEROTOXIN TYPE G.
FT DISULFID 116 133 BY SIMILARITY.
SQ SEQUENCE 258 AA; 29940 MW; E2982101701D012C CRC64;

Query Match 14.28; Score 175; DB 1; Length 258;
Best Local Similarity 23.28; Pred. No. 1.3e-06;
Matches 64; Conservative 57; Mismatches 91; Indels 64; Gaps 12;

QY 1 MKKINIKIYFIITVILISTYFTYHOSDKKDISNVKSD-----LLYATTIPYD 50
DB 1 MKKLSVITILILEIVFHNMYNAOPDKLDELNKVDYKKNKGTMGNWMLTSPPE 60
QY 51 YKDCRVNFTTHLTIDTOKYRGKDYISSEMSYEASQKFK-----RBDHYDV 98
DB 61 GRGV-----INSRQFLSHDLFFPIE--YKSYNEVTELENTLANNYDKKVDI 107
QY 99 FGL--FY-----ILNSHGEYIYGGITPAONKNVNHKLGNLFISGESQONLNK 146
DB 108 FGVPYFTCIIPKSEPDINONFGCCMYGGLTFENSSENERDKLI-TVQVTLDNQSLGFT 166
QY 147 ILEKDLVFOEIDFKIRKLMQNKRYDAT-SPYVSGRIEIGRKDGHQIDLFDSFNE. 205
DB 167 ITTNKNKVVTOELDYKARHMLTEKKLYEFGSAFESGGLKFTKKNNTSEWFDL----- 221
QY 206 GTRSDI--FAKYK-----DNRIIMKNKFSHFIDYL 233
DB 222 -PKKELVPYFYKFLNLYGDNKVDSKSIK-MEYFL 255

RESULT 10
ETC1_STAAU STANDARD; PRT; 266 AA.
AC P01552;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Enterotoxin type C-1 precursor (SEC1).
GN EMTCL.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88038352; PubMed=2823067;
RA Bohach G.A., Schlievert P.M.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
RT relatedness to other pyrogenic toxins.";
RL Mol. Gen. Genet. 209:15-20(1987).
RN [2]
RP SEQUENCE OF 28-266.
RX MEDLINE=83213327; PubMed=6189824;
RA Schmidt J.J., Spero L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";
RL J. Biol. Chem. 258:6300-6306(1983).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STAPHYLOCOCCAL ENTEROTOXINS CAUSE THE INTOXICATION
CC STAPHYLOCOCCAL FOOD POISONING SYNDROME.
CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN
CC FAMILY.
CC -----
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CC -----
DR EMBL: X05815; CAA29260.1; -.
DR PIR: S06356; ENSRCL.
DR HSSP: P34071; 1SB2.
DR InterPro: IPR006177; Bcrl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_08.
DR Pfam: PF02876; Staph_strep_tox_C; 1.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Enterotoxin; Toxin; Signal; Superantigen.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-1.
FT DISULFID 120 137
FT CONFLICT 177 177 D -> N (IN REF. 2).
SQ SEQUENCE 266 AA; 30546 MW; 3A7AB59A8986853B CRC64;

Query Match 13.98; Score 171.5; DB 1; Length 266;
Best Local Similarity 25.78; Pred. No. 2.4e-06;
Matches 67; Conservative 49; Mismatches 102; Indels 43; Gaps 12;

QY 1 MKKINIKIYFIITVILISTYFTYHOSDKK-----ISNVKSLV-AY 44
DB 1 MNKSRFISCVLILIALIIVFTPNVLAESQDPPEDELKSKTKGLMENNK--VLIDDH 58
QY 45 TTPDYKDCRVNFTHTL--NIDTOKYRGKDYISSEMSYEASQKFRDHDVYGLF 102
DB 59 YVSATFKVKS--VDKFLAHDLIYINISDKRLKYVD-KVKTLLNEGKAKKYKDEVYVYGSN 115
QY 103 YILNSH-----IG--EYTGGITPAONKNVNHKLGNLFISGESQONLNKLTLE 150
DB 116 YVNCYFSSKDNVKGKYGKTCMGYGITKHGHNFGNGLONVLI--RVYENKRNITSEF 173
QY 151 ----KDIYFOEIDFKIRKLMQNKRYD-ATSPYVSGRIEIGRKDGHQIDLFDSFNE 205
DB 174 VQTRKKSVTQAEELDKARHMLFNKNKLNLYEFNSSYEYIGYIKFIENNGTFYDMMAPAGD 233
QY 206 G-TRSDIFAKYKDNRIIMKN 225
DB 234 KFDQSKYLMYNDNKTVDSKS 254

RESULT 11
ETXB_STAAU STANDARD; PRT; 266 AA.
AC P01552;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Enterotoxin type B precursor (SEB).
GN ENTB.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86168029; PubMed=3957869;
RA Jones C.L., Khan S.A.;
RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus
RT aureus.";
RL J. Bacteriol. 166:29-33(1986).
RN [2]
RP SEQUENCE OF 40-91 FROM N.A.
RX MEDLINE=85298255; PubMed=3898073;
```


Db 166 DGNLSPDYQVQNNKVTQAQELDYLTRHLYVKNKKLYEFNNSPYETGYIKFIENENF-W 224

Oy 197 IDLFDSPNEG-TRSDIFAKYKDNRIIMKMFHSDIYL 233

Db 225 YDMMPAPGDKFQDSKYLAMINDKNKVDSDKVC-IEVYL 261

RESULT 12

SPFH_STRPY STANDARD; PRT; 236 AA.

AC Q9X5C8; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DE 15-SEP-2003 (Rel. 42, Last annotation update)

DE Exotoxin type H precursor (SPE H).

GN SPEH OR SPY1008.

OS Streptococcus pyogenes.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.

OX NCBI_TaxID=1314; [1]

RN SEQUENCE FROM N.A.

RC STRAIN=M15; MEDLINE=99093428; PubMed=9874566;

RA Profit T., Mofatt S.L., Berkahn C.J., Fraser J.D.;

RT "Identification and characterization of novel superantigens from Streptococcus pyogenes."

RL J. Exp. Med. 189:89-102(1999).

[2]

RN SEQUENCE FROM N.A.

RC STRAIN=SF370 / ATCC 700294 / Serotype M1; MEDLINE=21192684; PubMed=11296296;

RA Ferretti J.J., Mcshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K., Primeaux C., Segate S., Suvorov A.N., Kenton S., Lal H.S., Lin S.P., Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J., Ryan X., Clifton S.W., Roe B.A., McLaughlin R.;

RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."

RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).

CC -1- SUBUNIT: Binds to major histocompatibility complex class II beta chain.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- DISEASE: Mitogenic for human peripheral blood lymphocytes.

CC -1- SIMILARITY: BELONGS TO THE STAPHYLOCOCCAL/STREPTOCOCCAL TOXIN FAMILY.

CC -----

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CC -----

DR EMBL; AF124500; AAD30989.1; -

DR EMBL; AE006546; AAK33907.1; -

DR PDB; 1ET9; 24-MAY-00.

DR PDB; 1EU4; 24-MAY-00.

DR InterPro: IPR006123; Staph/Strep_toxin.

DR InterPro: IPR006126; Staph/Strep_tox.

DR InterPro: IPR006173; Staph_tox_OB.

DR Pfam: PF02876; Staph_strep_tox_C; 1.

DR Pfam: PF01133; Staph_strep_toxin; 1.

DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.

DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.

DR Toxin; Signal; Complete proteome; 3D-structure.

FT SIGNAL 1 32 POTENTIAL.

FT CHAIN 33 236 EXOTOXIN TYPE H.

SO SEQUENCE 236 AA; 27485 MW; 16352923907AD40D CRC64; -

Query Match 11.5%; Score 142; DB 1; Length 236;

Best Local Similarity 28.4%; Pred. No. 0.00038;

Matches 69; Conservative 41; Mismatches 99; Indels 34; Gaps 15;

Oy 2 KKI--NIKIVFII--TVLISYFT--YHQSDS--KKDISNKSDDLVAATTPYDKD 53

Db 12 KKIISMICISFLIYSNVQANSYNTNRNINLESLYHDSNLEAD---SIKNSP----- 63

Oy 54 CRNVESTHTLNDITQKRGKDYIISSEMSYE-ASQKFKDDHVDVGLF--YILNSHTG 110

Db 64 ---DIVTSHML---KYSVKDKNLVSFFEKDWISQEFK-DKEVDIALSAQVECECPGK 114

Oy 111 EY-IYSGITPAONNNKVAHKLGNLFISGESQONNNKIIIEKDIYFQELDFKRYKLM 169

Db 115 RYEAFGITPLTNSKEKIKVAVNW--DKSQQPMFTVKKPKVTAQVQEDIKRKLIR 172

Oy 170 NYKIY-DATSPYVSGRIEIGTKDGHQIDLFDSPNEGTRSDIFAKYKDNRIIMKMFH 228

Db 173 KYDIYNNRQKYSKGYTLTDLNSGDIYFDLIYTCN-GDENSMLKITSNNRIDSQF-H 230

Oy 229 FDI 231

Db 231 VDV 233

RESULT 13

NUOG_BUCAP STANDARD; PRT; 910 AA.

AC Q8K9Y2; 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE NADH-quinone oxidoreductase chain G (EC 1.6.99.5) (NADH dehydrogenase I, chain G) (NDH-1, chain G).

GN NUOG OR BUSG152.

OS Buchnera aphidicola (subsp. Schizaphis graminum).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Buchnera.

OX NCBI_TaxID=96794; [1]

RN SEQUENCE FROM N.A.

RC MEDLINE=22084549; PubMed=12089438;

RA Tamás I., Klasson L., Canhaeck B., Naeslund A.K., Eriksson A.-S., Wernegreen J.J., Sandstrom J.P., Moran N.A., Andersson S.G.E.;

RT "50 million years of genomic stasis in endosymbiotic bacteria."

RL Science 296:2376-2379(2002).

CC -1- FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and iron-sulfur (Fe-S) centers, to quinones in the respiratory chain.

CC Couples the redox reaction to proton translocation (for every two electrons transferred, four hydrogen ions are translocated across the cytoplasmic membrane), and thus conserves the redox energy in a proton gradient (By similarity).

CC -1- CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.

CC -1- COFACTOR: Binds 1 2Fe-2S cluster and 1 4Fe-4S cluster (Potential).

CC -1- SUBUNIT: Composed of 13 different subunits. Subunits nuoCD, E, F, and G constitute the peripheral sector of the complex (By similarity).

CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 75 kDa SUBUNIT FAMILY.

CC -----

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CC -----

DR EMBL; AE014091; AAM67720.1; -

DR InterPro: IPR000283; Complex1_75K.

DR InterPro: IPR001041; Ferredoxin.

DR Pfam: PF00111; fer2; 1.

DR Pfam: PF04879; Molybdop_Fe4S4; 1.

DR PROSITE: PS00641; COMPLEX1_75K_1; 1.

DR PROSITE: PS00642; COMPLEX1_75K_2; 1.

DR PROSITE: PS00643; COMPLEX1_75K_3; 1.

KW Oxidoreductase; NAD; Quinone; Metal-binding; Iron-sulfur; Iron; 2Fe-2S; 4Fe-4S; Complete proteome.

FT METAL 23 23 IRON-SULFUR (2FE-2S) (POTENTIAL).
 FT METAL 34 34 IRON-SULFUR (2FE-2S) (POTENTIAL).
 FT METAL 45 45 IRON-SULFUR (2FE-2S) (POTENTIAL).
 FT METAL 48 48 IRON-SULFUR (2FE-2S) (POTENTIAL).
 FT METAL 103 103 IRON-SULFUR (2FE-2S) (POTENTIAL).
 FT METAL 106 106 IRON-SULFUR (2FE-2S) (POTENTIAL).
 FT METAL 112 112 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 151 151 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 154 154 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 157 157 IRON-SULFUR (4FE-4S) (POTENTIAL).
 FT METAL 201 201 IRON-SULFUR (4FE-4S) (POTENTIAL).
 SO SEQUENCE 910 AA; 104358 MW; 7F50E2F296DA519 CRC64;

Query Match 7.8%; Score 96.5; DB 1; Length 910;
 Best Local Similarity 20.5%; Pred. No. 5.5;
 Matches 61; Conservative 41; Mismatches 93; Indels 103; Gaps 12;

QY 9 IVFIITVILSTYTYTHOSDKDISVKSDDLVAITTPYDKCR-----VNFS 59
 DB 64 IMSCMTVPIDGTIISINDTSKFRSRNIVELL--TNHPDCEVCCEGNGCHLDMTVM 120
 QY 60 TTHTL-NIDTOKYRGKDYISSEMSYASQ-----KFKRD---DHVDVFG---LF 102
 DB 121 TTHFRYRFRSKRTHKNOYLGSFIKHEMNCICGRCVRYRYADGTDLDVYANNNTY 180
 QY 103 Y-----INSHTEGY----- 113
 DB 181 FGRIEHCYLENEHSGNLEICPTGVFTDKTHSKYKRNKMDQVAPGICQNSICGNISIG 240
 QY 114 --YGGITPAQN--NKNVHKLGNLFISGESQONLNKIIIEKDIYVFOEIDFKIRKYL 168
 DB 241 ERVEIIRRIENRYHESINHYLICDLGRGYSHTLKN--PKRPILSKENDVNLNF-- 296
 QY 169 DNYKIYDASPYYGRIEIGTKDGKHQIDLEFDSNCEGTRSDIAKYNKRNIIIMKN 226
 DB 297 -NKAIETATNFOYKKNVIG-----GSIRSIENNALDELVEKKNF 358

RESULT 14
 ETP1_YABAM STANDARD; PRT: 635 AA.
 ID ETP1_YABAM
 AC Q90B97;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Early transcription factor 70 kDa subunit (VEF1 small subunit).
 OS BAR.
 OS Yaba monkey tumor virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Yatapoxvirus.
 OX NCBI_TaxID=38804;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Amano H., Morikawa S., Ueda Y., Miyamura T.;
 RT "Nucleotide sequence of the central 50kbp region of Yaba virus DNA";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ACTS WITH RNA POLYMERASE TO INITIATE TRANSCRIPTION FROM
 CC EARLY GENE PROMOTERS. A DNA-DEPENDENT ATPASE ACTIVITY IS
 CC ASSOCIATED WITH VEF1.
 CC -1- SUBUNIT: HETERODIMER OF A 70 kDa AND A 82 kDa SUBUNIT.
 CC -1- SIMILARITY: BELONGS TO THE VEF1 SUBFAMILY OF HELICASES.

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 CC
 CC EMBL: AB015885; BAA88798.1; -
 CC DR InterPro: IPR001410; DEAD.
 CC DR InterPro: IPR002464; DEAD_box.

DR InterPro: IPR001650; Helicase_C.
 DR InterPro: IPR00271; helicase_C.1.
 DR SMART: SM00487; DEXDC, 1.
 DR PROSITE: PS00690; DEAD_ATP_HELICASE, 1.
 KW Helicase; Transcription regulation; Activator; ATP-binding.
 FT NP_BIND 45 52 ATP (POTENTIAL).
 FT SITE 135 138 DEXH BOX.
 SO SEQUENCE 635 AA; 73289 MW; BFD459B5A1D1854 CRC64;

Query Match 7.7%; Score 95; DB 1; Length 635;
 Best Local Similarity 22.5%; Pred. No. 4.8;
 Matches 56; Conservative 36; Mismatches 81; Indels 76; Gaps 13;

QY 2 KKNIVKIVFIITVILSTYTYTHOSDKDISVKSDDLVAITTPYDKCRVNFS 59
 DB 272 KNNMNVSLAVIGQNFINNLDILQEDQKELYPLKSLNGILYDELT----- 319
 QY 60 TTHTLNIDTOKYRGKDYISSEMSYASQKRRDHYVFGFLYLSNHSHTGEYIGITP 119
 DB 320 --TLNI-SSKFK--YFIGKITSLTGKQ-----FIYFSNS---TYGGLI- 354
 QY 120 AQNNKVHKLGNLFISGESQONLNKIIIEKDIYVFOEIDFKIRKILMPNRYKYDATSP 179
 DB 355 ----IKYIMLSNGYSEYNSQGTNPKLNGKP-KTFAIYVSKMKSSLEDLVNYSOL- 407
 QY 180 YVSGRIEIGTKDGKHQIDLEFDSNCEGTRSDIAKYNKRNIIIMKN 222
 DB 408 -----NKDG--SQIMLFSSNIMSESYTLKEVINIMPTIPDFSQ--NQLIGRS 454
 QY 223 MKNFSHFDI 231
 DB 455 IRKFSYFDI 463

RESULT 15
 TEGU_HSV6U STANDARD; PRT: 2077 AA.
 ID TEGU_HSV6U
 AC P52340;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Large tegument protein.
 GN U31 OR HHRF1.
 OS Human herpesvirus (type 6 / strain Uganda-1102) (HHV6).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Betaherpesvirinae; Roseolovirus.
 OX NCBI_TaxID=10370;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Compels U.A., Nicholas J., Lawrence G., Jones M., Thomson B.J.,
 RA Martin M.E., Efsthaliou S., Craxton M., Macaulay H.A.;
 RT "The DNA sequence of human herpesvirus-6: structure, coding content,
 RT and genome evolution".
 RL Virology 209:29-51(1995).
 CC -1- FUNCTION: TEGUMENT PROTEIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL36,
 CC EBV-1 24, EBV BPLF1, HVS-1 64, VZV 22, AND HCMV UL48.

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 CC
 CC EMBL: X83413; CA58411.1; -
 CC DR InterPro: IPR006928; Herpes_teg_N.
 CC DR InterPro: IPR006928; Herpes_teg_N.
 CC DR Pfam: PF04843; Herpes_teg_N.1.
 SO SEQUENCE 2077 AA; 239946 MW; C1CA4BDC2650511 CRC64;

Query Match 7.6%; Score 94; DB 1; Length 2077;

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